OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/995,542

DATE: 12/05/2001
TIME: 11:50:30

Input Set : A:\00658Aseq.txt
Output Set: N:\CRF3\11212001\I995542.raw

ENTERED

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 3 <110> APPLICANT: Shutter, John
 4        Ulias, Laarni
 6 <120> TITLE OF INVENTION: ATP-Binding Cassette Transporter-Like Molecules and
 7        Uses Thereof
 9 <130> FILE REFERENCE: 00-658-A
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/995,542
C--> 12 <141> CURRENT FILING DATE: 2001-11-28
14 <150> PRIOR APPLICATION NUMBER: 60/253,520
15 <151> PRIOR FILING DATE: 2000-11-28
17 <160> NUMBER OF SEQ ID NOS: 24
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 6633
23 <212> TYPE: DNA
24 <213> ORGANISM: Mus musculus
26 <220> FEATURE:
27 <221> NAME/KEY: sig_peptide
28 <222> LOCATION: (1)..(138)
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(6504)
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37  1               5                   10                  15
39 tat cga cgg aga caa ccg atc caa cta cta gtg gag ttg ctt tgg ccc      96
40 Tyr Arg Arg Arg Gln Pro Ile Gln Leu Leu Val Glu Leu Leu Trp Pro
41                 20                  25                  30
43 ctc ttc ctc ttc ttc atc cta gtg gct gtc cgt cac tcc cac ccc cct     144
44 Leu Phe Leu Phe Phe Ile Leu Val Ala Val Arg His Ser His Pro Pro
45             35                  40                  45
47 ctg gag cat cac gaa tgc cac ttt cca aac aag cca tta cca tcg gcg     192
48 Leu Glu His His Glu Cys His Phe Pro Asn Lys Pro Leu Pro Ser Ala
49         50                  55                  60
51 ggc acg gtg ccc tgg ctg cag ggc ctt gtc tgc aac gta aac aac tcc     240
52 Gly Thr Val Pro Trp Leu Gln Gly Leu Val Cys Asn Val Asn Asn Ser
53  65                  70                  75                  80
55 tgc ttc cag cac cca acg cct ggc gag aag cct ggg gtc ctg agt aac     288
56 Cys Phe Gln His Pro Thr Pro Gly Glu Lys Pro Gly Val Leu Ser Asn
57                 85                  90                  95
59 ttt aag gat tcc ttg atc tcg agg ctc ctc gct gat acc cgc aca gtg     336
60 Phe Lys Asp Ser Leu Ile Ser Arg Leu Leu Ala Asp Thr Arg Thr Val
61                 100                 105                 110
63 ctc ggg ggc cac agc atc cag gac atg ctg gat gcc ctg ggg aaa ctg     384
64 Leu Gly Gly His Ser Ile Gln Asp Met Leu Asp Ala Leu Gly Lys Leu
65             115                 120                 125
67 atc ccc gtg ctc agg gca gtt gga ggt gga gca cga cca cag gag agt     432
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68  Ile Pro Val Leu Arg Ala Val Gly Gly Gly Ala Arg Pro Gln Glu Ser
69      130             135             140
71  gac cag ccg acc agt caa ggg tca gtg act aag ctt ctg gag aag atc    480
72  Asp Gln Pro Thr Ser Gln Gly Ser Val Thr Lys Leu Leu Glu Lys Ile
73  145             150             155             160
75  ctg caa agg gca tcc ctg gat cct gtg ctg ggt caa gcc cag gat tct    528
76  Leu Gln Arg Ala Ser Leu Asp Pro Val Leu Gly Gln Ala Gln Asp Ser
77              165             170             175
79  atg aga aag ttc tca gat gct atc agg gat ctt gcc cag gag ctc ctg    576
80  Met Arg Lys Phe Ser Asp Ala Ile Arg Asp Leu Ala Gln Glu Leu Leu
81          180             185             190
83  aca ctg ccc agc ctg atg gag ctc cga gct ttg ctg cgg agg ccc cga    624
84  Thr Leu Pro Ser Leu Met Glu Leu Arg Ala Leu Leu Arg Arg Pro Arg
85          195             200             205
87  ggg tca gct ggt tct ctg gag ctg gtt tcg gag gcc ctc tgc agt acc    672
88  Gly Ser Ala Gly Ser Leu Glu Leu Val Ser Glu Ala Leu Cys Ser Thr
89      210             215             220
91  aag gga ccc agc agt cca ggg ggc ctg tcc ctc aat tgg tac gaa gcc    720
92  Lys Gly Pro Ser Ser Pro Gly Gly Leu Ser Leu Asn Trp Tyr Glu Ala
93  225             230             235             240
95  aac cag ctt aat gag ttc atg ggg cca gag gtg gcc cct gcc ctg cct    768
96  Asn Gln Leu Asn Glu Phe Met Gly Pro Glu Val Ala Pro Ala Leu Pro
97              245             250             255
99  gac aac agt ctc agc cct gcc tgc tct gag ttt gtg ggg aca ctg gat    816
100 Asp Asn Ser Leu Ser Pro Ala Cys Ser Glu Phe Val Gly Thr Leu Asp
101             260             265             270
103 gac cac cct gtg tct cgg ctg ctc tgg agg cgc ctg aag cca ttg atc    864
104 Asp His Pro Val Ser Arg Leu Leu Trp Arg Arg Leu Lys Pro Leu Ile
105             275             280             285
107 ctc ggg aaa att ctc ttt gca cct gac aca aac ttc act cgg aag ctc    912
108 Leu Gly Lys Ile Leu Phe Ala Pro Asp Thr Asn Phe Thr Arg Lys Leu
109     290             295             300
111 atg gct cag gtg aac cag acc ttc gag gag ctg gct ctg ttg agg gac    960
112 Met Ala Gln Val Asn Gln Thr Phe Glu Glu Leu Ala Leu Leu Arg Asp
113 305             310             315             320
115 cta cac gaa ctc tgg ggg gtg ctg gga ccc cag atc ttc aac ttc atg   1008
116 Leu His Glu Leu Trp Gly Val Leu Gly Pro Gln Ile Phe Asn Phe Met
117             325             330             335
119 aat gac agt acc aac gtg gcc atg ctt cag agg ctt ctg gat gtg ggg   1056
120 Asn Asp Ser Thr Asn Val Ala Met Leu Gln Arg Leu Leu Asp Val Gly
121             340             345             350
123 ggc aca ggg cag agg cag cag aca ccc aga gcc cag aag aag ttg gag   1104
124 Gly Thr Gly Gln Arg Gln Gln Thr Pro Arg Ala Gln Lys Lys Leu Glu
125             355             360             365
127 gct atc aaa gac ttt ctg gat cct agt agg ggt ggc tac agc tgg cgg   1152
128 Ala Ile Lys Asp Phe Leu Asp Pro Ser Arg Gly Gly Tyr Ser Trp Arg
129     370             375             380
131 gag gcc cac gca gat atg gga cgc ctg gct gga atc cta gga caa atg   1200
132 Glu Ala His Ala Asp Met Gly Arg Leu Ala Gly Ile Leu Gly Gln Met
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133 385                       390                    395                        400
135 atg gag tgt gtg tcc ctg gac aag ctg gag gct gtg ccc tca gag gaa    1248
136 Met Glu Cys Val Ser Leu Asp Lys Leu Glu Ala Val Pro Ser Glu Glu
137             405                    410                    415
139 gct ctt gtg tcc cgt gcc ctg gag ctg ctg ggt gag cgc cgc ctc tgg    1296
140 Ala Leu Val Ser Arg Ala Leu Glu Leu Leu Gly Glu Arg Arg Leu Trp
141             420                    425                    430
143 gca ggc atc gtg ttc ctg agc cca gag cat cct ctg gac cca tcc gaa    1344
144 Ala Gly Ile Val Phe Leu Ser Pro Glu His Pro Leu Asp Pro Ser Glu
145             435                    440                    445
147 ctg tca tct cca gcc ctg agt cct ggc cac cta cga ttc aag att cga    1392
148 Leu Ser Ser Pro Ala Leu Ser Pro Gly His Leu Arg Phe Lys Ile Arg
149       450                    455                    460
151 atg gat atc gat gat gtc aca agg acc aat aag atc agg gac aag ttt    1440
152 Met Asp Ile Asp Asp Val Thr Arg Thr Asn Lys Ile Arg Asp Lys Phe
153 465                    470                    475                    480
155 tgg gac cca ggt ccg tca gca gat cct ttc atg gac ctt cgg tat gtg    1488
156 Trp Asp Pro Gly Pro Ser Ala Asp Pro Phe Met Asp Leu Arg Tyr Val
157             485                    490                    495
159 tgg gga ggc ttc gtg tac ctg cag gac ctg ctg gag cag gca gct gtg    1536
160 Trp Gly Gly Phe Val Tyr Leu Gln Asp Leu Leu Glu Gln Ala Ala Val
161             500                    505                    510
163 cga gtg ctc ggt ggc ggg aac tcc cgc aca ggt ctc tac ctg cag cag    1584
164 Arg Val Leu Gly Gly Gly Asn Ser Arg Thr Gly Leu Tyr Leu Gln Gln
165             515                    520                    525
167 atg cca cac ccc tgc tac gtg gat gat gtg ttc ctg cgg gtg ctg agc    1632
168 Met Pro His Pro Cys Tyr Val Asp Asp Val Phe Leu Arg Val Leu Ser
169       530                    535                    540
171 cgg tct ctg cct ctg ttt ctg act ctg gcc tgg att tat tcg gtg gcg    1680
172 Arg Ser Leu Pro Leu Phe Leu Thr Leu Ala Trp Ile Tyr Ser Val Ala
173 545                    550                    555                    560
175 ctc act gtg aag gcc gtg gtg cgt gag aaa gag aca cgg ctg cga gaa    1728
176 Leu Thr Val Lys Ala Val Val Arg Glu Lys Glu Thr Arg Leu Arg Glu
177             565                    570                    575
179 acc atg cgt gcg atg ggg ctg agc cgc gcg gtg ctc tgg ctt ggt tgg    1776
180 Thr Met Arg Ala Met Gly Leu Ser Arg Ala Val Leu Trp Leu Gly Trp
181             580                    585                    590
183 ttc ctc agc tgc ctg gga ccc ttc ctg gtc agc gct gcg ttg ctg gta    1824
184 Phe Leu Ser Cys Leu Gly Pro Phe Leu Val Ser Ala Ala Leu Leu Val
185             595                    600                    605
187 tta gtg ctt aag cta ggg aac atc ctt cct tac agc cac ccg gtt gta    1872
188 Leu Val Leu Lys Leu Gly Asn Ile Leu Pro Tyr Ser His Pro Val Val
189       610                    615                    620
191 atc ttc ctt ttc ttg gcg gcc ttc gcg gtg gcc acc gtc gct cag agt    1920
192 Ile Phe Leu Phe Leu Ala Ala Phe Ala Val Ala Thr Val Ala Gln Ser
193 625                    630                    635                    640
195 ttt ctg ctc agc gcc ttc ttc tcc agg gcc aat ctg gca gca gcc tgc    1968
196 Phe Leu Leu Ser Ala Phe Phe Ser Arg Ala Asn Leu Ala Ala Ala Cys
197             645                    650                    655
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199 ggg ggg ctc gcc tat ttt gcg ctc tat ctg ccc tac gta ctg tgt gtg   2016
200 Gly Gly Leu Ala Tyr Phe Ala Leu Tyr Leu Pro Tyr Val Leu Cys Val
201         660             665             670
203 gcc tgg cgc gag cgc ctg cac ctg ggc gga ctc tta gct gcg agc ctg   2064
204 Ala Trp Arg Glu Arg Leu His Leu Gly Gly Leu Leu Ala Ala Ser Leu
205         675             680             685
207 ctg tcc cct gta gcc ttt ggc ttt gga tgc gaa agc ctg gcg cta cta   2112
208 Leu Ser Pro Val Ala Phe Gly Phe Gly Cys Glu Ser Leu Ala Leu Leu
209         690             695             700
211 gag gag cag gga gac ggg gct cag tgg cac aat ttg ggc aca ggc ccc   2160
212 Glu Glu Gln Gly Asp Gly Ala Gln Trp His Asn Leu Gly Thr Gly Pro
213 705             710             715             720
215 gcg gag gac gtc ttc agc ctg gcc cag gtg tct gcc ttc ctg ttg ctt   2208
216 Ala Glu Asp Val Phe Ser Leu Ala Gln Val Ser Ala Phe Leu Leu Leu
217             725             730             735
219 gat gcc gtc atc tac ggc ctt gcc ctc tgg tac cta gag gct gtg tgc   2256
220 Asp Ala Val Ile Tyr Gly Leu Ala Leu Trp Tyr Leu Glu Ala Val Cys
221             740             745             750
223 cca ggc cag tat gga atc cct gaa cca tgg aat ttc cct ttt cgg agg   2304
224 Pro Gly Gln Tyr Gly Ile Pro Glu Pro Trp Asn Phe Pro Phe Arg Arg
225         755             760             765
227 agc tac tgg tgt gga cct ggg cct ccc aag agt tct gtc ttg gcc cct   2352
228 Ser Tyr Trp Cys Gly Pro Gly Pro Pro Lys Ser Ser Val Leu Ala Pro
229         770             775             780
231 gcc cca caa gat ccc aag gtt ctg gtg gaa gag cca ccc ctt ggc ctg   2400
232 Ala Pro Gln Asp Pro Lys Val Leu Val Glu Glu Pro Pro Leu Gly Leu
233 785             790             795             800
235 gtt cct ggt gtc tcc att cga ggc ctg aag aaa cat ttt cgt ggc tgt   2448
236 Val Pro Gly Val Ser Ile Arg Gly Leu Lys Lys His Phe Arg Gly Cys
237             805             810             815
239 ccg cag cca gcc ctg caa gga ctc aac ctt gac ttc tac gaa ggc cac   2496
240 Pro Gln Pro Ala Leu Gln Gly Leu Asn Leu Asp Phe Tyr Glu Gly His
241         820             825             830
243 atc act gcc ttt ttg ggt cac aac ggg gct ggc aag aca acc aca ctg   2544
244 Ile Thr Ala Phe Leu Gly His Asn Gly Ala Gly Lys Thr Thr Thr Leu
245         835             840             845
247 tcc att ttg agt ggt ctc ttc cca ccc agt agt ggc tcg gcc tcc atc   2592
248 Ser Ile Leu Ser Gly Leu Phe Pro Pro Ser Ser Gly Ser Ala Ser Ile
249 850             855             860
251 ctg ggc cat gat gta caa acc aac atg gca gcc atc cgg ccc cac ctg   2640
252 Leu Gly His Asp Val Gln Thr Asn Met Ala Ala Ile Arg Pro His Leu
253 865             870             875             880
255 ggc atc tgc ccg cag tac aat gtg ctg ttt gat atg ctg aca gtg gaa   2688
256 Gly Ile Cys Pro Gln Tyr Asn Val Leu Phe Asp Met Leu Thr Val Glu
257             885             890             895
259 gaa cat gtt tgg ttc tat ggc cgt ttg aaa ggc gtg agt gca gcc gcc   2736
260 Glu His Val Trp Phe Tyr Gly Arg Leu Lys Gly Val Ser Ala Ala Ala
261         900             905             910
263 atg ggc ccc gag cgg gaa cgt ctg ata cgg gat gtg ggg ctt acc ctc   2784
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Input Set : A:\00658Aseq.txt
Output Set: N:\CRF3\11212001\I995542.raw

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264 Met Gly Pro Glu Arg Glu Arg Leu Ile Arg Asp Val Gly Leu Thr Leu
265         915                 920                 925
267 aag cgg gac aca cag aca cgc cac ctc tct ggt gga atg cag aga aaa    2832
268 Lys Arg Asp Thr Gln Thr Arg His Leu Ser Gly Gly Met Gln Arg Lys
269         930                 935                 940
271 ctt tct gtg gcc att gcc ttt gtg ggt ggc tct cgt gtg gtc atc atg    2880
272 Leu Ser Val Ala Ile Ala Phe Val Gly Gly Ser Arg Val Val Ile Met
273 945                 950                 955                 960
275 gac gag ccc act gct ggt gtg gac ccc gct tcc cgc cgt ggc att tgg    2928
276 Asp Glu Pro Thr Ala Gly Val Asp Pro Ala Ser Arg Arg Gly Ile Trp
277                 965                 970                 975
279 gaa ttg cta ctt aag tac aga gaa ggt cgg aca ctg att ctc tcc act    2976
280 Glu Leu Leu Leu Lys Tyr Arg Glu Gly Arg Thr Leu Ile Leu Ser Thr
281                 980                 985                 990
283 cac cac ctg gat gag gca gag ctc ttg gga gat cgc gtg gcc atg gtg    3024
284 His His Leu Asp Glu Ala Glu Leu Leu Gly Asp Arg Val Ala Met Val
285         995                 1000                1005
287 gca ggt ggc tct ttg tgc tgc tgt ggg tcc ccg ctt ttc ttg cgc cga    3072
288 Ala Gly Gly Ser Leu Cys Cys Cys Gly Ser Pro Leu Phe Leu Arg Arg
289     1010                1015                1020
291 cac ttg ggc tgc ggt tac tac ctg acc ctg gtg aag agt tct cag tcc    3120
292 His Leu Gly Cys Gly Tyr Tyr Leu Thr Leu Val Lys Ser Ser Gln Ser
293 1025                1030                1035                1040
295 ctc gtc acc cat gat gct aag gga gac agt gag gac ccc aga cgg gaa    3168
296 Leu Val Thr His Asp Ala Lys Gly Asp Ser Glu Asp Pro Arg Arg Glu
297                 1045                1050                1055
299 aag aag tca gat ggc aat ggc agg acg tca gac aca gcg ttc aca cga    3216
300 Lys Lys Ser Asp Gly Asn Gly Arg Thr Ser Asp Thr Ala Phe Thr Arg
301         1060                1065                1070
303 gga acc tca gac aag agc aac cag gcc ccg gct cct ggc gcc gtt ccc    3264
304 Gly Thr Ser Asp Lys Ser Asn Gln Ala Pro Ala Pro Gly Ala Val Pro
305         1075                1080                1085
307 atc acc cca agc aca gcc cgg ata cta gag cta gtg cag cag cat gtg    3312
308 Ile Thr Pro Ser Thr Ala Arg Ile Leu Glu Leu Val Gln Gln His Val
309     1090                1095                1100
311 cct gga gca caa ctc gtg gag gac ctg ccc cat gag ctt ctg ctt gtg    3360
312 Pro Gly Ala Gln Leu Val Glu Asp Leu Pro His Glu Leu Leu Leu Val
313 1105                1110                1115                1120
315 cta ccc tat gcg ggg gcc ctg gat ggc agc ttc gcc atg gtc ttc cag    3408
316 Leu Pro Tyr Ala Gly Ala Leu Asp Gly Ser Phe Ala Met Val Phe Gln
317                 1125                1130                1135
319 gag ctg gat cag cag ctg gag ctc ctg ggt ctc aca ggc tac ggg atc    3456
320 Glu Leu Asp Gln Gln Leu Glu Leu Leu Gly Leu Thr Gly Tyr Gly Ile
321         1140                1145                1150
323 tcg gac acc aac ctg gag gag atc ttc cta aag gtg gtg gag gat gcg    3504
324 Ser Asp Thr Asn Leu Glu Glu Ile Phe Leu Lys Val Val Glu Asp Ala
325         1155                1160                1165
327 cac aga gaa ggt ggg gac tct aga ccg cag ctg cac ctt cgc aca tgc    3552
328 His Arg Glu Gly Gly Asp Ser Arg Pro Gln Leu His Leu Arg Thr Cys
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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/995,542**

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Input Set : **A:\00658Aseq.txt**
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L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9